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OM protein - protein search, using sw model

Run on: June 27, 2003, 18:03:05 ; Search time 23 Seconds

(without alignments)
640.178 Million cell updates/sec

Title: US-09-922-895-1

Perfect score: 1854

Sequence: 1 MTTSLDTVETFTSTYDDY.....LERTSSVSPSTAPELSYF 355

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1854	100.0	355 1	CKR3_HUMAN
2	1717	92.6	355 1	CKR3_CERAE
3	1706	92.0	355 1	CKR3_MACMU
4	1293	69.7	359 1	CKR3_MOUSE
5	1264	68.2	359 1	CKR3_RAT
6	1253.5	67.6	358 1	CKR3_CAVPO
7	1181.5	63.7	355 1	CKR1_HUMAN
8	1121.5	60.5	355 1	CKR1_MACMU
9	1114.5	60.1	355 1	CKR1_MOUSE
10	863.5	52.0	373 1	CKR2_RAT
11	955.5	51.5	373 1	CKR2_MOUSE
12	954	51.2	360 1	CKR2_MACMU
13	949.5	51.1	352 1	CKR5_MACMU
14	948	51.1	352 1	CKR5_HYLE
15	947.5	51.0	352 1	CKR5_CERAE
16	945.5	50.9	352 1	CKR5_PAPHA
17	944.5	50.9	352 1	CKR5_CERTO
18	943	50.8	354 1	CKR5_RAT
19	942.5	50.7	352 1	CKR5_TRAFH
20	940.5	50.7	352 1	CKR5_GORGO
21	940.5	50.7	352 1	CKR5_PYGBI
22	940.5	50.7	352 1	CKR5_PYGBI
23	940	50.7	354 1	CKR5_MOUSE
24	939.5	50.7	352 1	CKR5_PANTR
25	939.5	50.7	352 1	CKR5_PONPY
26	938.5	50.7	352 1	CKR5_TRAFH
27	938.5	50.6	352 1	CKR5_HUMAN
28	927.5	50.0	356 1	CKRV_MOUSE
29	886.5	47.8	374 1	CKR2_HUMAN
30	803.5	43.3	360 1	CKR4_HUMAN
31	780.5	42.1	360 1	CKR4_MOUSE
32	710.5	38.3	354 1	CKX1_RAT
33	703	37.9	356 1	CKR8_MACMU

34	698.5	37.7	354 1	C3X1_MOUSE
35	692.5	37.4	355 1	CKR8_HUMAN
36	684	36.9	355 1	C3X1_HUMAN
37	659	35.5	353 1	CKR6_MOUSE
38	579.5	31.3	384 1	CKR6_HUMAN
39	572	30.9	374 1	CKR6_MOUSE
40	565	30.5	367 1	CKR6_MOUSE
41	563	30.4	357 1	CKR9_HUMAN
42	541.5	29.2	378 1	CKR7_HUMAN
43	541	29.2	369 1	CKR9_MOUSE
44	529.5	28.6	378 1	CKD6_MOUSE
45	523.5	28.2	367 1	CKR3_MOUSE

ALIGNMENTS

RESULT 1
ID CKR3_HUMAN STANDARD: PRT; 355 AA.
AC P51677; Q15748; Q9ULY8;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR-3) (CCR3)
DE (CKR3) (Eosinophil eotaxin receptor).
GN CCR3 OR CCR3R3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Monocytes.
RX MEDLINE=96235044; PubMed=7622448;
RA Combadiere C., Ahuja S.K., Murphy P.M.;
RT "Cloning and functional expression of a human eosinophil CC chemokine
RT receptor.";
RL J. Biol. Chem. 270:16491-16494(1995).
RN [2]
RP ERRATUM.
RA Combadiere C., Ahuja S.K., Murphy P.M.;
RL J. Biol. Chem. 270:30235-30235(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96235044; PubMed=8642344;
RA Daugherty B.L., Sticiliano S.J., Demartino J.A., Malkowitz L.,
RT "Cloning, expression, and characterization of the human eosinophil
RT eotaxin receptor.";
RL J. Exp. Med. 183:2349-2354(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=96281895; PubMed=8676064;
RA Ponath P.D., Qin S., Post T.W., Wang J., Wu L., Gerard N.P.,
RA Newman W., Gerard C., Mackay C.R.;
RT "Molecular cloning and characterization of a human eotaxin receptor
RT expressed selectively on eosinophils.";
RL J. Exp. Med. 183:2737-2748(1996).
RN [5]
RP SEQUENCE FROM N.A.
RX Xiao L., Weiss S., Oari S., Rudolph D., Hodge T., Lai R.;
RT "Partial resistance to infection by syncytium-inducing primary HIV-1
RT in exposed uninfected individuals homozygous for CCR5 32bp deletion.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. AND VARIANT SER-218.
RX MEDLINE=21040311; PubMed=11196669;
RA Kato H., Tsuchiya N., Izumi S., Miyama M., Nakajima T., Kawasaki H.,
RA Hirai K., Tokunaga K.;
RT "New variations of human CC-chemokine receptors CCR3 and CCR4.";
RL Genes Immun. 1:97-104(1999).
CC -1- FUNCTION: Receptor for a C-C type chemokine. Binds to eotaxin,

Query Match	Best Local Similarity	100.0%:	Score 1854:	DB 1:	Length 355:
Matches 355:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:	
1	MTSLDVEVEGETSYDDVGLCEKADTRALMAQFVPLIXSLVETVGLIGNVVMVLLI	60			
1	MTSLDVEVEGETSYDDVGLCEKADTRALMAQFVPLIXSLVETVGLIGNVVMVLLI	60			
61	KYRLRLMTNTNYLLNLALSDLLFTVLPFWLHYHVGHWGHHGCKLLSGFYHRTGLXSE	120			
61	KYRLRLMTNTNYLLNLALSDLLFTVLPFWLHYHVGHWGHHGCKLLSGFYHRTGLXSE	120			
121	IFFIILLIDIDYLAIVHAFVFLRARTVFGYITSIVTGLVIALPFIETEEELPFE	180			
121	IFFIILLIDIDYLAIVHAFVFLRARTVFGYITSIVTGLVIALPFIETEEELPFE	180			
181	TLCSALPDEPDVYSWRHRTLMRTIFCLVLPPLVMAICYTGIIKTLRCPSKKYKAIRL	240			
181	TLCSALPDEPDVYSWRHRTLMRTIFCLVLPPLVMAICYTGIIKTLRCPSKKYKAIRL	240			
241	IFVIMAFVEFIWTPYNAVILISVOSILFSGNDCESKRLDVMVTEVIAVSHCCMNPVI	300			
241	IFVIMAFVEFIWTPYNAVILISVOSILFSGNDCESKRLDVMVTEVIAVSHCCMNPVI	300			
241	IFVIMAFVEFIWTPYNAVILISVOSILFSGNDCESKRLDVMVTEVIAVSHCCMNPVI	300			

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OY      301 YAFGERRKTLRHFHRLMLHGRIPLFPESELENTSSVSTAPELSIYF 355
        |||
DB      301 YAFGERRKTLRHFHRLMLHGRIPLFPESELENTSSVSTAPELSIYF 355

                .RESULT 2
ID       CKR3_CERAE          STANDARD;          PRT;          355 AA.
AC       P56492;
DT       15-JUL-1998 (Rel. 36, Created)
DT       15-JUL-1998 (Rel. 36, Last sequence update)
DT       30-MAY-2000 (Rel. 39, Last annotation update)
DE       C-C chemokine receptor type 3 (C-C CRK-3) (CC-CR-3) (CCR-3) (CCR3)
DE       (CKR3).
GN       CKR3 OR CMKBRR.
OS       Cercopithecus aethiops (Green monkey) (Grivet).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC       Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciinae;
OC       Cercopithecidae; Cercopithecus.
OX       NCBI_TaxID=9534;
RN       [1]
RP       SEQUENCE FROM N.A.
RA       Sol N., Treboutte C., Gomas E., Fercchal F., Allison M.;
RL       Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
CC       -1 FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,
CC       MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC       INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC       -1 SUBCELLULAR LOCATION: Integral membrane protein.
CC       -1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC       -----
CC       This SWISS-PROT entry is copyright. It is produced through a collaboration
CC       between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC       or send an email to license@isb-sib.ch).
CC       -----
DR       EMBL; Y13775; CAN74106.1; -.
DR       InterPro; IPRO000276; GPCR_Rhodospn.
DR       InterPro; IPRO01230; Prenyl_site.
DR       Pfam; PF00001; 7tm_1; 1.
DR       PRINTS; PR00237; GPCRRHODOPSN.
DR       PROSITE; PS00237; G_PROTEIN_RECPT_FL1; 1.
DR       PROSITE; PS00262; G_PROTEIN_RECPT_FL2; 1.
KW       G-protein coupled receptor; Transmembrane.
FT       DOMAIN              1           34     EXTRACELLULAR (POTENTIAL).
FT       TRANSMM            35           62     CYTOPLASMIC (POTENTIAL).
FT       DOMAIN            63           72     CYTOPLASMIC (POTENTIAL).
FT       TRANSMM            73           93     2 (POTENTIAL).
FT       DOMAIN            94          107     EXTRACELLULAR (POTENTIAL).
FT       TRANSMM           108          129     3 (POTENTIAL).
FT       DOMAIN           130          146     CYTOPLASMIC (POTENTIAL).
FT       TRANSMM           147          171     4 (POTENTIAL).
FT       DOMAIN           172          203     EXTRACELLULAR (POTENTIAL).
FT       TRANSMM           204          223     5 (POTENTIAL).
FT       DOMAIN           224          239     CYTOPLASMIC (POTENTIAL).
FT       TRANSMM           240          264     6 (POTENTIAL).
FT       DOMAIN           265          281     EXTRACELLULAR (POTENTIAL).
FT       TRANSMM           282          305     7 (POTENTIAL).
FT       DOMAIN           306          355     CYTOPLASMIC (POTENTIAL).
FT       DISULFD            106          183     BY SIMILARITY.
SQ       SEQUENCE          355 AA;  40830 MW;  44F7A5EFEBB978FF CRC64;

Query Match      92.6%; Score 1717; DB 1; Length 355;
Best Local Similarity 92.1%; Pred. No. 7.6e-91;
Matches 327; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

OY      1 MTSIDIVETGTGSYYDDGVLCEKADPTALMAQFVPLXSLVFYGLGNVVVMILI 60
        |||||
DB      1 MTSISLVYETGPTSYDDMGKLCEKAQVGALINQFPPLTSLVFYGLGNVVVMILI 60

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OY 61 KYRRLKIMNTIYLNLAIISDLFLVTLPRMIVHVRGHNWFGHGKCKLISGFYHTGLYSE 120
DB 61 KYRRLKIMNTIYLNLAIISDLFLVTLPRMIVHVRGHNWFGHGKCKLISGFYHTGLYSE 120
OY 121 IFFIILLTDRIYLAIVHAFALRARTVGTGITSITWGLAVLAALPEFIYETEELFEE 180
DB 121 IFFIILLTDRIYLAIVHAFALRARTVGTGITSITWGLAVLAALPEFIYETEELFEE 180
OY 181 TLCSALYPEDVYSNRHFTLMTIFCGLVPLLVNACVYTGIIKTLRCPSKKKYAIRL 240
DB 181 TLCSALYPEDVYSNRHFTLMTIFCGLVPLLVNACVYTGIIKTLRCPSKKKYAIRL 240
OY 241 IFVIMAVFEFTFPYVNAIILSSYQSILFENDCKSRKHLDMVLTVEVIAISHCCNMPYI 300
DB 241 IFVIMAVFEFTFPYVNAIILSSYQSILFENDCKSRKHLDMVLTVEVIAISHCCNMPYI 300
OY 301 YAFVGERFRKYLHFFRHLMLHGRYIPFLPSEKLERISVSPSTAEPDELSTVF 355
DB 301 YAFVGERFRKYLHFFRHLMLHGRYIPFLPSEKLERISVSPSTAEPDELSTVF 355

RESULT 3
CKR3_MACMU STANDARD; PRT: 355 AA.
ID CKR3_MACMU
AC P56483:
DT 15-JUL-1998 (rel. 36, Created)
DT 15-JUL-1998 (rel. 36, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR3)
DE (CCR3).
GN CCR3 OR CCKBR3.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_Taxid=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT Identification and comparison of eleven rhesus macaque chemokine
RT receptors.*;
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98118446; PubMed=9454694;
RA Sol N., Treboute C., Gomas E., Ferchal F., Shacklett B., Alizon M.;
RT The rhesus macaque CCR3 chemokine receptor is a cell entry cofactor
RT for HIV-2, but not for HIV-1.*;
RL Virology 240:213-220(1998).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN,
CC MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF017283; AAB70527.1; -
CC EMBL: Y13776; CAA74107.1; -
CC InterPro: IPR000276; GPCR_Rhodopsn.
CC Pfam: PF00001; 7tm1.1.
CC PRINTS: PR00237; GPCR_RHOOPSN.
CC PROSITE: PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
CC PROSITE: PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
CC G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 35 62 1 (POTENTIAL).
FT DOMAIN 63 72 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 93 2 (POTENTIAL).
FT DOMAIN 94 107 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 108 129 3 (POTENTIAL).
FT DOMAIN 130 146 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMAIN 172 203 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 204 223 5 (POTENTIAL).
FT DOMAIN 224 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMAIN 265 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMAIN 306 335 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183 BY SIMILARITY.
FT CONFLICT 180 180 K -> E (IN REF. 2).
FT CONFLICT 202 202 K -> R (IN REF. 2).
SQ SEQUENCE 355 AA: 40805 MW: 52716 E949709F CRC64;

Query Match 92.0%; Score 1706; DB 1; Length 355;
Best Local Similarity 91.3%; Pred. No. 3.2e-90;
Matches 324; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

OY 1 MTSIDTVETFEFTSYDDVGLGCEKADRALMAQFVPPYLSVFTVGLGNVVMILI 60
DB 1 MTSIDTVETFEFTSYDDVGLGCEKADRALMAQFVPPYLSVFTVGLGNVVMILI 60
OY 61 KYRRLKIMNTIYLNLAIISDLFLVTLPRMIVHVRGHNWFGHGKCKLISGFYHTGLYSE 120
DB 61 KYRRLKIMNTIYLNLAIISDLFLVTLPRMIVHVRGHNWFGHGKCKLISGFYHTGLYSE 120
OY 121 IFFIILLTDRIYLAIVHAFALRARTVGTGITSITWGLAVLAALPEFIYETEELFEE 180
DB 121 IFFIILLTDRIYLAIVHAFALRARTVGTGITSITWGLAVLAALPEFIYETEELFEE 180
OY 181 TLCSALYPEDVYSNRHFTLMTIFCGLVPLLVNACVYTGIIKTLRCPSKKKYAIRL 240
DB 181 TLCSALYPEDVYSNRHFTLMTIFCGLVPLLVNACVYTGIIKTLRCPSKKKYAIRL 240
OY 241 IFVIMAVFEFTFPYVNAIILSSYQSILFENDCKSRKHLDMVLTVEVIAISHCCNMPYI 300
DB 241 IFVIMAVFEFTFPYVNAIILSSYQSILFENDCKSRKHLDMVLTVEVIAISHCCNMPYI 300
OY 301 YAFVGERFRKYLHFFRHLMLHGRYIPFLPSEKLERISVSPSTAEPDELSTVF 355
DB 301 YAFVGERFRKYLHFFRHLMLHGRYIPFLPSEKLERISVSPSTAEPDELSTVF 355

RESULT 4
CKR3_MOUSE STANDARD; PRT: 359 AA.
ID CKR3_MOUSE
AC P51678:
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE Probable C-C chemokine receptor type 3 (C-C CKR-3) (CC-CKR-3) (CCR3)
DE 2) (MIP-1 alpha RL2).
GN CCR3 OR CCKBR3 OR CCKBR1L2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SV.
RX MEDLINE=96072806; PubMed=7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA Gerard C.;
RT Molecular characterization of two murine eosinophil beta chemokine
RT receptors.*;
RL J. Immunol. 155:5299-5305(1995).
RN [2]

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SEQUENCE FROM N.A.

RC STRAIN-128/SVJ; PubMed=7542241;

RA Gao J.-L., Murphy P.M.;

RT "Cloning and differential tissue-specific expression of three mouse beta chemokine receptor-like genes, including the gene for a functional macrophage inflammatory protein-1 alpha receptor.";

RL J. Biol. Chem. 270:17494-17501(1995).

CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN, MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: DETECTED IN SKELETAL MUSCLE AND IN TRACE AMOUNTS IN LEUKOCYTES.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL: U29677; AAA86118.1; -

DR EMBL: U28406; AAA89155.1; -

DR MGI:104616; Gmbr112.

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCRHHODPSN.

DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.

DR PROSITE: PS50262; G_PROTEIN_REC_P1_2; 1.

KM G-protein coupled receptor; Transmembrane.

FT DOMAIN 1 38

FT TRANSSEM 39 64

FT DOMAIN 65 68

FT TRANSSEM 69 95

FT DOMAIN 96 111

FT TRANSSEM 112 133

FT DOMAIN 134 150

FT TRANSSEM 151 175

FT DOMAIN 176 201

FT TRANSSEM 202 227

FT DOMAIN 228 243

FT TRANSSEM 244 268

FT DOMAIN 269 285

FT TRANSSEM 286 309

FT DOMAIN 310 359

FT DISULFID 110 187

FT CONFLICT 270 270

SO SEQUENCE 359 AA; 41825 MW; AC11ED6E283CEAF CMC64;

Query Match 69.7%; Score 1293; DB 1; Length 359;

Best Local Similarity 70.4%; Pred. No. 7e-67;

Matches 245; Conservative 41; Mismatches 62; Indels 0; Gaps 0;

QY 8 VETGTSYVDDVGLCEKADPTALMAQFVPLISVFTVGLGVVYVMLITRRKRI 67

DB 12 VESSETPYEEMAPPEKVAIKELGSLPLPLSLVEIIGLNNMVAALLIKYRKLOI 71

QY 68 MTNIIYLAISDLFTLVTFPMIHYVGNHVFHGHCCKLLSGFYHGYKSEIFILL 127

DB 72 MTNIIYLAISDLFTLVTFPMIHYVGNHVFHGHCCKLLSGFYHGYKSEIFILL 131

QY 128 TIDRYLAIVHVAFLRARTVTEGVTSIVTWGLAVLALPEFIYEETEEETLCALY 187

DB 132 TIDRYLAIVHVAFLRARTVTEGVTSIVTWGLAVLALPEFIHESQDSGSCSPRY 191

QY 188 PEDVYVSRHFRHTIICLVPLVLAICYTGIIKTLCPSSKKYKAIKILFVMAV 247

DB 192 PEGEEDSWKRHFRHTIICLVPLVLAICYTGIIKTLCPSSKKYKAIKILFVMAV 251

QY 248 FEIWTPEYNAVLISVTSQSLFGNDCERSKHLDMVLTVEIVAVSHCCMNVIYAFVGR 307

DB 252 FEIWTPEYNAVLISVTSQSLFGNDCERSKHLDMVLTVEIVAVSHCCMNVIYAFVGR 311

QY 308 FRKYLRFHFRHILMHILGRYIPCLPSEKLETTSSVSPSTAPELISV 355

DB 312 FRKYLRFHFRHILMHILGRYIPCLPSEKLETTSSVSPSTAPELISV 359

RESULT 5

CC CR3_RAT STANDARD; PRT; 359 AA.

AC 054814; OS5169; (rel. 39, Created)

DT 30-MAY-2000 (rel. 39, Last sequence update)

DT 30-MAY-2000 (rel. 39, Last annotation update)

DE C-C chemokine receptor type 3 (C-C CR-3) (CC-CR-3) (CCR-3) (CCR3)

GN CCR3 OR CCR3R3.

OS Rattus norvegicus (rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_Taxid=10116;

RM [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RC STRAIN-Mistar; TISSUE-Spleen;

RX MEDLINE-98318173; PubMed=9653467;

RA Jiang Y., Salazar M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., Defebvre C.M., Pennell N.A., Strell W.J., Harrison J.K.;

RT "Chemokine receptor expression in cultured glia and rat experimental allergic encephalomyelitis.";

RL J. Neuroimmunol. 86:1-12(1998).

RM [2]

RP SEQUENCE FROM N.A.

RC STRAIN-Mistar; TISSUE-Spleen;

RA Harrington P.M., Newton D.J., Coleman J.W., Flanagan B.F.;

RL Submitted (Jan-1998) to the EMBL/Genbank/DDBJ databases.

CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO EOTAXIN, MCP-3, MCP-4 AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN SPLEEN BUT NOT IN ASTROCYTES OR MICROGLIA.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL: AF003954; AAC03337.1; -

DR EMBL: Y13400; CAAT3830.1; -

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS: PR00237; GPCRHHODPSN.

DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.

DR PROSITE: PS50262; G_PROTEIN_REC_P1_2; 1.

KM G-protein coupled receptor; Transmembrane.

FT DOMAIN 1 43

FT TRANSSEM 44 64

FT DOMAIN 65 74

FT TRANSSEM 75 95

FT DOMAIN 96 112

FT TRANSSEM 113 133

FT DOMAIN 134 154

FT TRANSSEM 155 175

FT DOMAIN 176 206

FT TRANSSEM 207 227

FT DOMAIN 228 243

FT TRANSSEM 244 264

FT DOMAIN 265 288

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

POTENTIAL.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

POTENTIAL.

EXTRACELLULAR (POTENTIAL).

Query	Match	Best Local Similarity	Score	DB 1	Length	Gaps
DR	PF000031; 7tm.1; 1.					
DR	PRINTS; PR00237; GPCR_HODOPSIN					
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1.1; 1.					
DR	PROSITE; PS50262; G-PROTEIN_RECEP_F1.2; 1.					
KW	G-protein coupled receptor; Transmembrane					
FT	DOMAIN 1 43					
FT	TRANSSEM 44 64					
FT	DOMAIN 65 74					
FT	TRANSSEM 75 95					
FT	DOMAIN 96 112					
FT	TRANSSEM 113 133					
FT	DOMAIN 134 154					
FT	TRANSSEM 155 175					
FT	DOMAIN 176 206					
FT	TRANSSEM 207 227					
FT	DOMAIN 228 243					
FT	TRANSSEM 244 264					
FT	DOMAIN 265 287					
FT	TRANSSEM 288 308					
FT	DOMAIN 309 358					
SEQ	SEQUENCE 358 AA; 41623 MW; 7873F8B7A3BC670 CAC64;					
Query Match	67.68; Score 1253.5; DB 1; Length 358;					
Best Local Similarity	68.08; Pred. No. 1.2e-64;					
Matches 234; Conservative 45; Mismatches 64; Indels 1; Gaps 1;						
QY	12 GTTSYVDYDGLGKADKADTRALMAQFVPLRYSLVTVGLGVNVMILIKYRRLRIMNI 71					
DB	16 GTTFYDYDFRPOPCRKVSITDGLAQPLSLFSLVIFVGLGNITVIVLTKYQKLKIMNI 75					
QY	72 YLNLAIASDLLFLVTLPEFWIHVYRGHNVFSGHKCKLSGFRHGLYSEIFIIILTD 131					
DB	76 YLLMLAISDLLFLFTLPFPFWYHVMKNKVFHFPMCKIKITSGLYVGLFSEIFIIILTD 135					
QY	132 YLALVHVEALRAETVFGVITSTVTCGLAVIALPERIFETELREPTICSLXPEDT 191					
DB	136 YLALVHVEAFALRTVTFGIIITVITWLAVALALPEWFGTGFSEVLCGSPYPERK 195					
QY	192 VYSRHRHFTMTFFCLVLPLLVAAICVTGIIKTLRPSKKRKAIRLIFVIMAVFIF 251					
DB	196 EHHMKRQALRMNIFGLALPLLIMICVTGIIKTLRPSKKRKAIRLIFVIMAVFIF 255					
QY	252 WTPNNVALISYSIILFGNDCSEKHLDMVLTVEYVAISHCCNPYIVAFVGEREKY 311					
DB	256 WTPNNALLISAF-DLSFLDCCSEKQDLMKAKHTEVFAHHCINPIIVAFVGERFOY 314					
QY	312 LRHFPHRLMLHLCGYITPELSEKLEKTSVSPGAPDELISVF 355					
DB	315 LRHFLHRNVMLSKYITPELSEKLEKSSISPSSGDELSYVF 358					
RESULT 7						
CRKL_HUMAN	STANDARD; PRT; 355 AA.					
AC	P32246;					
DT	01-OCT-1993 (Rel. 27, Created)					
DT	01-OCT-1993 (Rel. 27, Last sequence update)					
DT	16-OCT-2001 (Rel. 40, Last annotation update)					
DE	C-C chemokine receptor type 1 (C-C-CR-1) (CC-CR-1) (CCR-1) (CCR1)					
DE	(Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)					
DE	(RANTES-R) (HM145) (LD78 receptor).					
GN	CCR1 OR CCR1 OR CCR1.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
OX	NCBI_TaxID:9606;					
RP	SEQUENCE FROM N.A.					
FX	MEDLINE-93161416; PubMed-7679328;					
RA	Neote K., DiGregorio D., Mak J.Y., Horuk R., Schall T.J.;					
RT	"Molecular cloning, functional expression, and signaling					
RT	characteristics of a C-C chemokine receptor.";					
TL	Cell 72:415-425(1993).					

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RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-93240122; PubMed-7683036;
RA Gao J.-L., Kuhn D., Tiffany H.L., McDermott D., Li X., Francke U.,
RT Murphy P.M.;
RT "Structure and functional expression of the human macrophage
RT inflammatory protein 1 alpha/RANTES receptor."
RL J. Exp. Med. 177:1421-1427(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Monocytes;
RX MEDLINE-94092629; PubMed-7505609;
RA Nomura H., Nielsen B.W., Matsushima K.;
RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative
RT leukocyte chemotactic peptide receptors."
RL Int. Immunol. 5:1239-1249(1993).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1 DELTA, RANTES, AND MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-
CC BETA OR MCP-1 AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING
CC THE INTRACELLULAR CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING
CC STEM CELL PROLIFERATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT HEMATOPOIETIC
CC CELLS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; L09230; AAA58408.1; -
DR EMBL; L10918; AAA36543.1; -
DR EMBL; D10925; BAA01723.1; -
DR PIR; A45177; A45177.
DR GENE; HGNC:1602; CCR1.
DR MIM; 601159;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34
FT TRANSMEM 35 60
FT DOMAIN 61 64
FT TRANSMEM 65 91
FT TRANSMEM 92 107
FT TRANSMEM 108 129
FT DOMAIN 130 146
FT TRANSMEM 147 171
FT TRANSMEM 172 197
FT TRANSMEM 198 223
FT DOMAIN 224 239
FT TRANSMEM 240 264
FT DOMAIN 265 281
FT TRANSMEM 282 305
FT DOMAIN 306 355
FT CARBOHYD 5
FT DISULFID 106 183
FT CONFLICT 337
FT SEQUENCE 355 AA; 41172 MW; B2C100FED275983 CRC64;
Query Match 63.7%; Score 1181.5; DB 1; Length 355;
Best Local Similarity 63.2%; Pred. No. 1.4e-60;
Matches 222; Conservative 57; Mismatches 71; Indels 1; Gaps 1;
OY 6 DTVEFTGTSYYD-DVGLLCEKADTRALMAQFVPLVLTGVLGNVVVVMLIKRR 64
Db 5 NTFEDYPTTFEFYDGDATPCQKVNBRARAGQALLPLVSLVAVIGLVGNIIVLVLYQKR 64

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OY 65 LRIHTNYILNIAISDLLFLVTLPPWIHYRGHNVFGHGCKLLSGEYRTGLYSEIFFI 124
Db 65 LKNTSIYILNIAISDLLFLFLPWIIDYKLDKDDVFGDAMCKILSGEYRTGLYSEIFFI 124
OY 125 ILTIDRLAYIAHAFARARVTRGVTSITVWGLAVLAALPEITFETELFEETICS 184
Db 125 ILTIDRLAYIAHAFARARVTRGVTSITVWGLAVLAALPEITFETELFEETICS 184
OY 185 ALYPEDTVYSWRHFRTLTIRFCLVPLLVNAICVYTGILTKLRCPKSKRYKAILRIFY 244
Db 185 LAFPHESLRKMLPQALKNLFGVLPPLVIMICTTGITKILRRPNKRSKAVLLIFY 244
OY 245 MAVEFIETPTVVAAILLSYOSILFGDCKSKHLDVWLVEYIAVSHCCNPIYIAV 304
Db 245 MIIFLFMTPTVVAAILLSYOSILFGDCKSKHLDVWLVEYIAVSHCCNPIYIAV 304
OY 305 GRPFKRYLRHPRHRLNHLGRTYIPFLSEKTEKRTSSPSPAEELISVF 355
Db 305 GRPFKRYLRHPRHRLNHLGRTYIPFLSEKTEKRTSSPSPAEELISVF 355
OY 305 GERFKRYLRHPRHRLNHLGRTYIPFLSEKTEKRTSSPSPAEELISVF 355
Db 305 GERFKRYLRHPRHRLNHLGRTYIPFLSEKTEKRTSSPSPAEELISVF 355

RESULT 8
ID CCR1_MACMU STANDARD; PRT; 355 AA.
AC P56482;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CCR-1) (CCR-1) (CCR1).
GN CCR1 OR CCRBR1.
OS Macaca mulatta (rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21354176; PubMed-11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC RANTES, MCP-3 AND, LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
CC PROLIFERATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; AF017282; AAB70526.1; -
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 34
FT TRANSMEM 35 60
FT DOMAIN 61 64
FT TRANSMEM 65 91
FT TRANSMEM 92 107
FT TRANSMEM 108 129
FT DOMAIN 130 146
FT CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 147 171 4 (POTENTIAL).
FT DOMA1N 172 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 223 5 (POTENTIAL).
FT DOMA1N 224 239 5 (POTENTIAL).
FT TRANSMEM 240 264 6 (POTENTIAL).
FT DOMA1N 265 281 6 (POTENTIAL).
FT TRANSMEM 282 305 7 (POTENTIAL).
FT DOMA1N 306 335 7 (POTENTIAL).
FT CARBOHYD 5 5 CYTOPLASMIC (POTENTIAL).
FT DISULFID 106 183 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 355 AA; 41198 MW; 41CAEA7CC19D23D4 CRC64;

Query Match 60.5%; Score 1121.5; DB 1; Length 355;
Best Local Similarity 60.4%; Pred. No. 3,4e-57;
Matches 216; Conservative 55; Mismatches 77; Indels 7; Gaps 2;

OY 8 VETFGTTSYD-----DVG--LLCEKADTRALMAQFVPLYSIVFTVGLGNVVMILL 60
DB 1 MEPTNTEDYDMDTEPDYGDATPCCHKYNERAIIAQLLPPLYSIVFTVGLGNVVMILLV 60
OY 61 KYRRLRLMTNIVLNTAISDLFLVPLPFWIHVYRGHNVFGHGMCKILSGFHTGLYSE 120
DB 61 QYRLKMTNIVLNTAISDLFLVPLPFWIHVYRGHNVFGHGMCKILSGFHTGLYSE 120
OY 121 IFFIILITDRYLAIVHAFALARKYTFEGVITSYWGAVLAALPEFTFYETEEELFEE 180
DB 121 IFFIILITDRYLAIVHAFALARKYTFEGVITSYWGAVLAALPEFTFYETEEELFEE 180
OY 121 IFFIILITDRYLAIVHAFALARKYTFEGVITSYWGAVLAALPEFTFYETEEELFEE 180
DB 121 IFFIILITDRYLAIVHAFALARKYTFEGVITSYWGAVLAALPEFTFYETEEELFEE 180
OY 181 TICSALYPEDVYVSMRHFHTLMTIFCLVPLVMAICGIIKTLRCPSKKRYKRI 240
DB 181 HSNHIFPYSFOQMKIFOLKTLNGLVPLVMAICGIIKTLRCPSKKRYKRI 240
OY 241 IFVIMAFLEFMTPYNAVALLSYQSILFGNDCERSKHLDMVLYEVIAVSHCCMPVI 300
DB 241 IFVIMAFLEFMTPYNAVALLSYQSILFGNDCERSKHLDMVLYEVIAVSHCCMPVI 300
OY 301 YAVGGERFKYLAHFRHLMHGRITPFLPSEKLETSVSPSTAPELSIYF 355
DB 301 YAVGGERFKYLAHFRHLMHGRITPFLPSEKLETSVSPSTAPELSIYF 355
DB 301 YAVGGERFKYLAHFRHLMHGRITPFLPSEKLETSVSPSTAPELSIYF 355

+ RESULT 9
CRKL MOUSE STANDARD; PRT; 355 AA.
ID CRKL MOUSE STANDARD; PRT; 355 AA.
AC P51675;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-C chemokine receptor type 1 (C-C CKR-1) (CCR-1) (CCR1)
DE (Macrophage inflammatory protein-1 alpha receptor) (MIP-1alpha-R)
DE (RANTES-R).
GN CCR1 OR CCR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID-10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-129/SV; TISSUE-Peritoneal macrophage;
RX MEDLINE-96072806; PubMed-7594543;
RA Post T.W., Bozic C.R., Rothenberg M.E., Luster A.D., Gerard N.,
RA Gerard C.;
RT "Molecular characterization of two murine eosinophil beta chemokine
RT receptors."
RL J. Immunol. 155:5299-5305(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-129/SV;
RX MEDLINE-93340346; PubMed-7542241;
RA Gao J.-L., Murphy P.M.;
RT "Cloning and differential tissue-specific expression of three mouse
RT beta chemokine receptor-like genes, including the gene for a
RT functional macrophage inflammatory protein-1 alpha receptor."

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RL J. Biol. Chem. 270:17494-17501(1995).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC RANTES, AND LESS EFFICIENTLY, TO MIP-1-BETA OR MCP-1 AND
CC SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR
CC CALCIUM IONS LEVEL. RESPONSIBLE FOR AFFECTING STEM CELL
CC PROLIFERATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: DETECTED IN THE HEART, SPLEEN, LUNG,
CC PERITONEAL EXUDATE CELLS AND LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@sdb-sdb.ch).
CC
DR EMBL; U29678; AAA86119.1;
DR EMBL; U28404; AAA89153.1;
DR MGI; 104618; Cmkrl1.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1;
DR PROSITE: PS0262; G-PROTEIN_RECPT_F2_1;
KW G-protein coupled receptor; Transmembrane.
FT TRANSMEM 1 34
FT DOMA1N 35 60
FT TRANSMEM 61 64
FT TRANSMEM 65 91
FT DOMA1N 92 107
FT TRANSMEM 108 129
FT DOMA1N 130 146
FT TRANSMEM 147 171
FT TRANSMEM 172 197
FT TRANSMEM 198 223
FT TRANSMEM 224 239
FT TRANSMEM 240 264
FT DOMA1N 265 281
FT TRANSMEM 282 305
FT TRANSMEM 306 335
FT DOMA1N 306 335
FT DISULFID 106 183
FT CONFILCT 55
SQ SEQUENCE 355 AA; 40901 MW; FCE9FEFF0E638B1 CRC64;

Query Match 60.1%; Score 1114.5; DB 1; Length 355;
Best Local Similarity 58.4%; Pred. No. 8,4e-57;
Matches 205; Conservative 63; Mismatches 82; Indels 1; Gaps 1;

OY 6 DIVEFGTTSYD-----DVGILCEKADTRALMAQFVPLYSIVFTVGLGNVVMILLIYRR 64
DB 5 DFTFAVYPTTFEPYDSDTPCKTRAVRFGACGLPPLYSIVFTVGLGNVVMILLIYRR 64
OY 65 LRIMTNTIVLNTAISDLFLVPLPFWIHVYRGHNVFGHGMCKILSGFHTGLYSEIFFI 124
DB 65 LQSWTSIYLFNLAIVHAFALARKYTFEGVITSYWGAVLAALPEFTFYETEEELFEE 124
OY 125 ILITIDRYLAIVHAFALARKYTFEGVITSYWGAVLAALPEFTFYETEEELFEE 184
DB 125 ILITIDRYLAIVHAFALARKYTFEGVITSYWGAVLAALPEFTFYETEEELFEE 184
OY 185 ALYEPEDVYVSMRHFHTLMTIFCLVPLVMAICGIIKTLRCPSKKRYKRI 244
DB 185 PHFPYKSLKQMKRQALKINLGLILPLVMAICGIIKTLRCPSKKRYKRI 244
OY 245 MAVFEFTPYNAVALLSYQSILFGNDCERSKHLDMVLYEVIAVSHCCMPVIYAFV 304
DB 245 TLLEFLLMTPTNYSVFSAPQDVLFTNQCQSKHLDMVLYEVIAVSHCCMPVIYAFV 304
OY 305 GERFRKTLRHFHRLMHGRITPFLPSEKLETSVSPSTAPELSIYF 355

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DB 305 GEFWKYRLQLEFORHVAIPLAKMLPFLSDQLERTSSISPSGHEHLSAGF 355

RESULT 10

CR2_RAT STANDARD: PRT: 373 AA.

AC 055193:

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE C-C chemokine receptor type 2 (C-C CR-2) (CC-CR-2) (CCR-2) (CCR2).

GN CCR2 OR CCR2R.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OK NCBI_TaxID=10116;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RX MEDLINE=96318173; PubMed=9655467;

RA Jiang Y., Salafraza M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K., deLelbe C.M., Pennell N.A., Strelt W.J., Harrison J.K.;

RT "Chemokine receptor expression in cultured glia and rat experimental allergic encephalomyelitis.";

RL J. Neuroimmunol. 86:1-12(1998).

CC -1- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5 CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND MACROPHAGES.

CC -1- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----

DR EMBL; U77349; AAC03242.1; -

DR InterPro: IPR000276; GPCR_Rhodopsn.

DR Pfam: PF00001; 7tm.1; 1.

DR PRINTS: PR00237; GPCR_RHODOPSN.

DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.

DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.

KW G-Protein coupled receptor; Transmembrane.

FT DOMAIN 1 60 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 61 81 POTENTIAL.

FT DOMAIN 82 91 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 92 112 POTENTIAL.

FT DOMAIN 113 128 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 129 149 POTENTIAL.

FT DOMAIN 150 170 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 171 191 POTENTIAL.

FT DOMAIN 192 220 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 221 241 POTENTIAL.

FT DOMAIN 242 256 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 257 277 POTENTIAL.

FT DOMAIN 278 301 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 302 322 POTENTIAL.

FT DOMAIN 323 373 CYTOPLASMIC (POTENTIAL).

FT DISULFID 126 203 BY SIMILARITY.

FT SEQUENCE 373 AA; 42763 MW; 2E7B012F5D6FD09 CRC64;

Query Match Score 963.5; DB 1; Length 373;

Best Local Similarity 53.0%; Pred. No. 3e-48;

Matches 187; Conservative 65; Mismatches 92; Indels 9; Gaps 7;

QY 4 SLIDVEFGTSTY-YDVGLICEKADFTALMAQFVPPLYSIVFTVGLGNVYVWILLIKY 62

DB 25 STQELDEGATTPYDD-GEPCHTSVKQIGAMWLPPLYSIVFTVGLGNVYVWILLISC 83

QY 63 RRLRIITLYLNLINLAISDLFLVTLPTFMHYVGNWYFGHGMCKLISGFTGLYSFEL 122

DB 84 KKLKSMTDIYENLNLISDLFLTLPLFMARVA-ANEMWFGNLMCLFLGVIHIGVGGIF 142

QY 123 FILLITIDRYLAIVAVARLARKYVTEGYTSYTWGLAVLAALPEFIYETEELEPTEL 182

DB 143 FILLITIDRYLAIVAVARLARKYVTEGYTSYTWGLAVLAALPEFIYETEELEPTEL 202

QY 183 CSALPEDEPVSWRPHLRLMTIFCLVPLVMAICYGIITKLRCPS-KKKYAIRLI 241

DB 203 GCPYTP--TI--WKRFQIMRNILSLPLVAVICIGILTTLPRCKNEKRRARVRI 258

QY 242 FVIMAVFIETWTPYVAVALLSSYOSILFGNDCERSKHDLVLAIVTEYVASHCCANPYIT 301

DB 259 FAIMIVYELFWTPYVAVALLSSYOSILFGNDCERSKHDLVLAIVTEYVASHCCANPYIT 318

QY 302 AFVGERFRKYLRFHFRHLMLHGRITPPLSEKLERTSSV-SPSTABEELSI 353

DB 319 AFVGERFRKYLRFHFRHLMLHGRITPPLSEKLERTSSV-SPSTABEELSI 371

RESULT 11

CR2_MOUSE STANDARD: PRT: 373 AA.

AC P51683; 061172;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE C-C chemokine receptor type 2 (C-C CR-2) (CC-CR-2) (CCR-2) (CCR2)

DE (JE/FIC receptor) (MCP-1 receptor).

DE CCR2 OR CCR2R.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OK NCBI_TaxID=10090;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=96205938; PubMed=8631787;

RA Boring L., Gosling J., Montecclaro F.S., Lusis A.J., Teou C.-L., Charo I.F.;

RT "Molecular cloning and functional expression of murine JE (monocyte chemoattractant protein 1) and murine macrophage inflammatory protein 1alpha receptors: evidence for two closely linked C-C chemokine receptors on chromosome 9.";

RL J. Biol. Chem. 271:7551-7558(1996).

RN (2)

RP SEQUENCE FROM N.A.

RC STRAIN=BALE/C;

RX MEDLINE=96216064; PubMed=8662823;

RA Kurihara T., Bravo R.;

RT "Cloning and functional expression of mCCR2, a murine receptor for the C-C chemokines JE and FIC.";

RL J. Biol. Chem. 271:11603-11606(1996).

RN (3)

RP SEQUENCE FROM N.A.

RX MEDLINE=97026720; PubMed=8872898;

RA Heesen M., Tanabe S., Berman M.A., Yoshizawa I., Luo Y., Kim R., Post T.W., Gerard C., Dorf M.E.;

RT "Mouse astrocytes respond to the chemokines MCP-1 and KC, but reverse transcriptase-polymerase chain reaction does not detect mRNA for the KC or new MCP-1 receptor.";

RL J. Neurosci. Res. 45:382-391(1996).

CC -1- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5 CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES, BUT NOT IN NONHEMATOPOIETIC CELL LINES.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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DR EMBL; U47035; AAC52453.1; -
DR EMBL; U51717; AAC52557.1; -
DR EMBL; U56819; AAC52784.1; -
DR MGI; MGI:106185; Cdkbr2.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOPOPSN.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
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FT TRANSMEM 84 93
FT TRANSMEM 94 114
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OY 133 LAIHAVALARATYEGVITISYWGIAVLAALPEFIETFEELFEELTCSALYPEDTV 192
DB 140 LAIHAVALARATYEGVITISYWGIAVLAALPEFIETFEELFEELTCSALYPEDTV 196
OY 193 YSMRFEHLRTMIFCTVPLVMAICVGIITLRCDS-KKKYKAIPLIFMIVFEE 251
DB 197 -GWNFEHIMNITLGLVPLIMVIGSILTLCKRKKRHRVRLIFITMIVFEE 255
OY 252 WTPYVAILLSSYOSILGNDCKSKHDLVLAIVTEVIAVSHCCNMPVIAVGERFRY 311
DB 256 WTPYVAILLSSYOSILGNDCKSKHDLVLAIVTEVIAVSHCCNMPVIAVGERFRY 315
OY 312 LRHFHRLMHLGRTYFPLSEKER-TSSVSPSTAPPELSI 353
DB 316 LMFPRKITYRKFCQCFYREIVDVTSTWTFSTAOEVSV 358

RESULT 13
CKRS_MACMU
ID CKRS_MACMU STANDARD; PRT: 352 AA.
AC P79436; 002746;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CCR-5) (CCR-5) (CCRS).
GN CCR5 OR CCR5P.
OS Macaca mulatta (rhesus macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca;
OX NCBI_TaxID:9544, 9541, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=97184592; PubMed=9032394;
RA Marcon L., Choe H., Martin K.A., Farzan M., Ponath P.D., Wu L.,
RA Newman W., Gerard N., Gerard C., Sodroski J.;
RT "Utilization of C-C chemokine receptor 5 by the envelope
RT glycoproteins of a pathogenic simian immunodeficiency virus,
RT siymac239."
RL J. Virol. 71:2522-2527(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=Indian macaque;
RX MEDLINE=97213934; PubMed=9060623;
RA Chen Z., Zhou P., Ho D.D., Landau N.R., Marx P.A.;
RT "Genetically divergent strains of simian immunodeficiency virus use
RT CCR5 as a coreceptor for entry."
RL J. Virol. 71:2705-2714(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta;
RX MEDLINE=21354176; PubMed=11461684;
RA Margulies B.J., Hauer D.A., Clements J.E.;
RT "Identification and comparison of eleven rhesus macaque chemokine
RT receptors."
RL AIDS Res. Hum. Retroviruses 17:981-986(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta, M.fascicularis, and M.nemestrina;
RX MEDLINE=97268687; PubMed=9108095;
RA Edinger A.L., Amodee A., Miller K., Doranz B.J., Endres M.,
RA Sharon M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,
RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;
RT "Differential utilization of CCR5 by macrophage and T cell tropic
RT simian immunodeficiency virus strains."
RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1 ALPHA,
CC MIP-1 BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR

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CC DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: U77672; AAC51109.1; -
DR EMBL: U73739; AAC51158.1; -
DR EMBL: U96762; AAC34132.1; -
DR EMBL: AF005660; AAB62554.1; -
DR EMBL: AF005661; AAB62555.1; -
DR EMBL: AF005662; AAB62556.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G-PROTEIN_RECP.F1.1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECP.F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT DOMAIN 59 68
FT TRANSMEM 69 89
FT DOMAIN 90 102
FT TRANSMEM 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT DOMAIN 167 198
FT TRANSMEM 199 218
FT DOMAIN 219 235
FT TRANSMEM 236 260
FT DOMAIN 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFD 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 15 15
FT CARBOHYD 268 268
FT CONFLICT 241 241
FT CONFLICT 292 292
SQ SEQUENCE 352 AA; 40507 MW; 58B9C685909FACB2 CRC64;
Query Match 51.2%; Score 949.5; DB 1; Length 352;
Best Local Similarity 54.5%; Pred. No. 1.8e-47;
Matches 181; Conservative 58; Mismatches 90; Indels 3; Gaps 3;
OY 24 CEKADTALMAQVFPYSLVETVGLGNNVVVLLITYRRLRINTNTYLLNATSDLE 83
DB 20 COKINVKIARLRLPLPSVIFRFGVNIIVLLINCKRKHSKTDITLLNATSDLE 79
OY 84 LVLPFWIHVYGNHNVFGHGCKLLSGFRTGLYSEIFITLLTIDRYLAIVNAVFAIR 143
DB 80 LLTVFPMHAYAA -QMDFGNTMCQLTGVLGFSGFIEFTLLIDRYLAIVNAVFAIR 138
OY 144 ARTVFGVITISYWGIAVLAALPEFIETFEELFEELTCSALYPEDTVYSKRHHITRM 203
DB 139 ARTVFGVITISYWGIAVLAALPEFIETFEELFEELTCSALYPEDTVYSKRHHITRM 198
OY 204 TFCVPLPLVVAICTYGIKTLRCPS-KKKYKAIPLIFMIVFEEFTMYPYVAIILS 262
DB 199 VILGVLPLVVAICTYGIKTLRCPS-KKKYKAIPLIFMIVFEEFTMYPYVAIILS 258
OY 263 SYOSILGNDCKSKHDLVLAIVTEVIAVSHCCNMPVIAVGERFRYLRHFHRLM 322
DB 259 TFOEFGGLNCSNRDLQAVTVETLGMTHCCINPIIYAFVGEFRNYLLVFPQHLAK 318

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OY 323 HLGRTYPLPSEKERTSSV-SPSTAPELSTI 353
DB 319 RFCRCSIFQOEAPERASSVYTRSTGEISV 350

RESULT 14
ID CCR5_HYLL STANDARD: PRT: 352 AA.
AC 097883;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C-CCR-5) (CCR-5) (CCR5).
GN Hylobates leucogenys (White-cheeked gibbon).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hylodactylidae; Hylobates.
OX NCBI_TaxID=61853;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RT "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL: AF075451; AAD19863.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm.1.1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN_RECPT_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT DOMAIN 1 30
FT TRANSMEM 31 58
FT TRANSMEM 59 68
FT TRANSMEM 69 89
FT TRANSMEM 90 102
FT DOMAIN 103 124
FT DOMAIN 125 141
FT TRANSMEM 142 166
FT TRANSMEM 167 198
FT TRANSMEM 199 218
FT TRANSMEM 219 235
FT TRANSMEM 236 260
FT TRANSMEM 261 277
FT TRANSMEM 278 301
FT DOMAIN 302 352
FT DISULFID 101 178
FT MOD_RES 3 3
FT MOD_RES 10 10
FT MOD_RES 14 14
FT MOD_RES 14 14
SQ SEQUENCE 352 AA; 40445 MW; 4F8EAF344CEB7C91 CRC64;

Query Match 51.18; Score 948; DB 1; Length 352;
Best Local Similarity 52.98; Pred. No. 2.1e-47;
Matches 181; Conservative 62; Mismatches 93; Indels 6; Gaps 4;
OY 17 YD--DVGLCEKADTRALMAQFVPLYSLVFTVGLGNVYVWILIKYRRLRLMTNTNYL 73

DB 10 YDIYDSEPOKINVOIARLLPPLYSLVFIFGVGNMVLIVLINCKRLKSMFTDIYL 69
OY 74 LNLAIIDLFLVTLPEPHHYVRGNWVPGHCKMLLSGFYHTGXSEFFILLTIDRYL 133
DB 70 LNLAIISDLFFLLVPEFAHATAA-OMDFGNMCOVLGLVIFGFSGLFFILLTIDRYL 128
OY 134 AIHAVPALRARVTFGVITSIVTWGLAVLAALFEETFEETFEETLCSALYEDPTVY 193
DB 129 AIHAVPALRKARVTFGVITSIVTWGLAVLAALFEETFEETFEETLCSALYEDPTVY 188
OY 194 SWRHFTLRMTIFELVPLVMAICYGIITLIDRCS-KKKYAIRLIFYNAVFIFW 252
DB 189 FKNRQTLKIYILVPLVMAICYGIITLIDRCS-KKKYAIRLIFYNAVFIFW 248
OY 253 TPYVAVILSTYOSILGNCDESKHLDVWLVTEVLAISHCQNPVYAVFGRRPRL 312
DB 249 APYIVILLNTFOEFGLNCSNRLDOAQVETLGMTHCCINPIITAVGKERFNYL 308
OY 313 RHFFRHLLMHLGRYIPFLPSEKERTSSV-SPSTAPELSTI 353
DB 309 LVFQKHAKRFFCCSIFQOEAPERASSVYTRSTGEISV 350

RESULT 15
ID CCR5_CERAE STANDARD: PRT: 352 AA.
AC P56493;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE C-C chemokine receptor type 5 (C-C-CCR-5) (CCR-5) (CCR5).
GN Cercopithecus aethiops (Green monkey) (Giveti).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98001387; PubMed=934322;
RA Kulmann S.E., Platt E.J., Kozak S.L., Kabat D.;
RT "Polymorphisms in the CCR5 genes of African green monkeys and mice
implicate specific amino acids in infections by simian and human
immunodeficiency viruses.";
RL J. Virol. 71:8642-8656(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Murayama Y., Matsunaga S., Inoue-Murayama M.;
RT "CDNA sequence of African green monkey CCR-5 chemokine receptor
gene.";
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
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CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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DR EMBL: U83324; AAC51795.1;
DR EMBL: U83325; AAC51796.1;
DR EMBL: AB015944; BAA31328.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.

DR	PIRAME: PF00001; 7cml; 1.	DR	PRINTS: P800237; GPCR RHODOPSIN.
DR	PROSITE: PS00237; G-PROTEIN RECP_F1.1; 1.	DR	PROSITE: PS00262; G-PROTEIN RECP_F1.2; 1.
KW	G-Protein coupled receptor; Glycoprotein; Sulfation; Polymorphism.	KW	
FT	DOMAIN 1 30	FT	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 31 58	FT	1 (POTENTIAL).
FT	DOMAIN 59 68	FT	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 69 89	FT	2 (POTENTIAL).
FT	DOMAIN 90 102	FT	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 103 124	FT	3 (POTENTIAL).
FT	DOMAIN 125 141	FT	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 142 166	FT	4 (POTENTIAL).
FT	DOMAIN 167 198	FT	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 199 218	FT	5 (POTENTIAL).
FT	DOMAIN 219 235	FT	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 236 260	FT	6 (POTENTIAL).
FT	DOMAIN 261 277	FT	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 278 301	FT	7 (POTENTIAL).
FT	DOMAIN 302 352	FT	CYTOPLASMIC (POTENTIAL).
FT	DISULFID 101 178	FT	BY SIMILARITY.
FT	MOD_RES 3 3	FT	SULFATION (BY SIMILARITY).
FT	MOD_RES 10 10	FT	SULFATION (BY SIMILARITY).
FT	MOD_RES 15 15	FT	SULFATION (BY SIMILARITY).
FT	VARIANT 14 14	FT	N -> Y.
FT	VARIANT 352 352	FT	F -> L.
SEQ	SEQUENCE 352 AA: 40561 MW: 7552690C72EC29A CRC64;		